

# SEQUENCE LISTING

<110> Tait, Jonathan F.

Brown, David S.

<120> Annexin Derivatives with Endogenous Chelation Sites

<130> uofw-1-13841

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<170> PatentIn Ver. 2.0

<210> 1

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(981)

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act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg	96
Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg	
20 25 30	

aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg	144
Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu	
35 40 45	

ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt	192
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50 55 60	

aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta	240
Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu	
65 70 75 80	

act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg	288
Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg	

ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336  
 Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
 100 105 110

aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa 384  
 Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg 432  
 Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
 130 135 140

gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg 480  
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 145 150 155 160

gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa 528  
 Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
 165 170 175

gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt 576  
 Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
 180 185 190

aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga 624  
 Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
 195 200 205

agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca 672  
 Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
 210 215 220

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 Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
 225 230 235 240

gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc 768  
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 245 250 255

tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat 816  
 Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
 260 265 270

gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg 864  
 Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

285

ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat-- 912  
 Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
 290 295 300

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960  
 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
 305 310 315 320

ctg ctc tcc gga gaa gat gac 981  
 Leu Leu Ser Gly Glu Asp Asp  
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&lt;210&gt; 2

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

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Met Ala Cys Gly Gly Gly His Met Ala Gln Val Leu Arg Gly Thr Val  
 1 5 10 15

Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg  
 20 25 30

Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu  
 35 40 45

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe  
 50 55 60

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
 65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
 85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
 130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu  
145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala  
245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu  
275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
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Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
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Leu Leu Ser Gly Glu Asp Asp  
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Thr	Asp	Phe	Pro	Gly	Phe	Asp	Glu	Arg	Ala	Asp	Ala	Glu	Thr	Leu	Arg	
			20					25					30			
aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg 144																
Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Glu	Ser	Ile	Leu	Thr	Leu	
		35					40					45				
ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192																
Leu	Thr	Ser	Arg	Ser	Asn	Ala	Gln	Arg	Gln	Glu	Ile	Ser	Ala	Ala	Phe	
		50				55					60					
aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta 240																
Lys	Thr	Leu	Phe	Gly	Arg	Asp	Leu	Leu	Asp	Asp	Leu	Lys	Ser	Glu	Leu	
		65			70				75					80		
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Thr	Gly	Lys	Phe	Glu	Lys	Leu	Ile	Val	Ala	Leu	Met	Lys	Pro	Ser	Arg	
			85					90					95			
ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336																
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Leu	Arg	Ala	Ile	Lys	Gln	Val	Tyr	Glu	Glu	Glu	Tyr	Gly	Ser	Ser	Leu	
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	145				150					155				160		
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			245					250					255				
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 35 40 45

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe  
 50 55 60

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
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Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
 85 90 95

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 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
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Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
 165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
 180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
 195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
 210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
 225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala  
 245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
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Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu  
 275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
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Leu Leu Ser Gly Glu Asp Asp  
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 35 40 45

ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt 192  
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 50 55 60

aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta 240  
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 85 90 95

ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca 336  
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 100 105 110



aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa	384
Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu	
115 120 125	
ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg	432
Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu	
130 135 140	
gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg	480
Glu Asp Asp Val Val Glu Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu	
145 150 155 160	
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Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu	
165 170 175	
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180 185 190	
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Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg	
195 200 205	
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Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser	
210 215 220	
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Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu	
225 230 235 240	
gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc	768
Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala	
245 250 255	
tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat	816
Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp	
260 265 270	
gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg	864
Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu	
275 280 285	
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Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr	
290 295 300	

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg 960  
 Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
 305 310 315 320

ctg ctc tcc gga gaa gat gac 981  
 Leu Leu Ser Gly Glu Asp Asp  
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<210> 6  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
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Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu  
 35 40 45

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe  
 50 55 60

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
 65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
 85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
 130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu  
 145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
 165 170 175

Ala	Gln	Val	Glu	Gln	Asp	Ala	Gln	Ala	Leu	Phe	Gln	Ala	Gly	Glu	Leu			
			180					185					190					
Lys	Trp	Gly	Thr	Asp	Glu	Glu	Lys	Phe	Ile	Thr	Ile	Phe	Gly	Thr	Arg			
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Ser	Val	Ser	His	Leu	Arg	Lys	Val	Phe	Asp	Lys	Tyr	Met	Thr	Ile	Ser			
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Asp	His	Thr	Leu	Ile	Arg	Val	Met	Val	Ser	Arg	Ser	Glu	Ile	Asp	Leu			
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Phe	Asn	Ile	Arg	Lys	Glu	Phe	Arg	Lys	Asn	Phe	Ala	Thr	Ser	Leu	Tyr			
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Ser	Met	Ile	Lys	Gly	Asp	Thr	Ser	Gly	Asp	Tyr	Lys	Lys	Ala	Leu	Leu			
305					310					315					320			
Leu	Leu	Ser	Gly	Glu	Asp	Asp												
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## SEQUENCE LISTING

<110> Tait, Jonathan  
Brown, David

<120> ANNEXIN DERIVATIVE WITH ENDOGENOUS CHELATION SITES

<130> UOFW-1-13841

<140> US 09/324,096

<141> 1999-06-01

<160> 12

<170> PatentIn version 3.0

<210> 1

<211> 981

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(981)

<400> 1

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Met Ala Cys Gly Gly Gly His Met Ala Gln Val Leu Arg Gly Thr Val

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5

10

15

act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg

96

Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg

20

25

30

aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg

144

Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu

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40

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ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt

192

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55

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aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta

240

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu

65

70

75

80

act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg

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85

90

95

ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca

336

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr

100

105

110

aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa

384

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu

115

120

125

ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg

432

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu

130

135

140

gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg

480

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu

145

150

155

160

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528

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu

165

170

175

gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt

576

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu

180

185

190

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624

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

195

200

205

agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca

672

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser

210

215

220

gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta

720

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu

225

230

235

240

gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc

768

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala

245

250

255

tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat

816

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp

260

265

270

gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg

864

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

285

ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat

912

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr

290

295

300

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg

960

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu

305

310

315

320

ctg ctc tcc gga gaa gat gac

981

Leu Leu Ser Gly Glu Asp Asp

325

&lt;210&gt; 2

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

Met	Ala	Cys	Gly	Gly	Gly	His	Met	Ala	Gln	Val	Leu	Arg	Gly	Thr	Val
1			5						10					15	

Thr	Asp	Phe	Pro	Gly	Phe	Asp	Glu	Arg	Ala	Asp	Ala	Glu	Thr	Leu	Arg
			20					25					30		

Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Glu	Ser	Ile	Leu	Thr	Leu
		35				40						45			

Leu	Thr	Ser	Arg	Ser	Asn	Ala	Gln	Arg	Gln	Glu	Ile	Ser	Ala	Ala	Phe
	50					55					60				



Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu  
145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala  
245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu  
 275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
 290 295 300

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
 305 310 315 320

Leu Leu Ser Gly Glu Asp Asp  
 325

<210> 3  
 <211> 981  
 <212> DNA  
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<220>  
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48  
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act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg

96  
 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg

20 25 30

aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg

144  
 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu

35

40

45

ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt

192

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe

50

55

60

aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta

240

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu

65

70

75

80

act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg

288

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg

85

90

95

ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca

336

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr

100

105

110

aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa

384

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu

115

120

125

ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg

432

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu

130

135

140

gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg

480

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu

145

150

155

160

gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa

528

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu

165

170

175

gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt

576

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu

180

185

190

aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga

624

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

195

200

205

agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca

672

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser

210

215

220

gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta

720

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu

225

230

235

240

gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc

768

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala

245

250

255

tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat

816

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp

260

265

270

gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg

864

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

285

ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat

912

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr

290

295

300

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg

960

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu

305

310

315

320

ctg ctc tcc gga gaa gat gac

981

Leu Leu Ser Gly Glu Asp Asp

325

<210> 4  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens

&lt;400&gt; 4

Met	Ala	Gly	Gly	Cys	Gly	His	Met	Ala	Gln	Val	Leu	Arg	Gly	Thr	Val
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Thr	Asp	Phe	Pro	Gly	Phe	Asp	Glu	Arg	Ala	Asp	Ala	Glu	Thr	Leu	Arg
			20					25					30		

Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Glu	Ser	Ile	Leu	Thr	Leu
		35					40					45			

Leu	Thr	Ser	Arg	Ser	Asn	Ala	Gln	Arg	Gln	Glu	Ile	Ser	Ala	Ala	Phe
	50					55					60				

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
 65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
 85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
 130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu  
 145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
 165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
 180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
 195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
 210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
 225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala  
 245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
 260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu  
 275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
 290 295 300

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
 305 310 315 320

Leu Leu Ser Gly Glu Asp Asp  
 325

<210> 5  
 <211> 981  
 <212> DNA  
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<220>  
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act gac ttc cct gga ttt gat gag cgg gct gat gca gaa act ctt cgg

96  
 Thr Asp Phe Pro Gly Phe Asp Glu Arg Ala Asp Ala Glu Thr Leu Arg

20 25 30

aag gct atg aaa ggc ttg ggc aca gat gag gag agc atc ctg act ctg

144  
 Lys Ala Met Lys Gly Leu Gly Thr Asp Glu Glu Ser Ile Leu Thr Leu



35

40

45

ttg aca tcc cga agt aat gct cag cgc cag gaa atc tct gca gct ttt

192

Leu Thr Ser Arg Ser Asn Ala Gln Arg Gln Glu Ile Ser Ala Ala Phe

50

55

60

aag act ctg ttt ggc agg gat ctt ctg gat gac ctg aaa tca gaa cta

240

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu

65

70

75

80

act gga aaa ttt gaa aaa tta att gtg gct ctg atg aaa ccc tct cgg

288

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg

85

90

95

ctt tat gat gct tat gaa ctg aaa cat gcc ttg aag gga gct gga aca

336

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr

100

105

110

aat gaa aaa gta ctg aca gaa att att gct tca agg aca cct gaa gaa

384

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu

115

120

125

ctg aga gcc atc aaa caa gtt tat gaa gaa gaa tat ggc tca agc ctg

432

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu

130

135

140

gaa gat gac gtg gtg ggg gac act tca ggg tac tac cag cgg atg ttg

480

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu

145

150

155

160

gtg gtt ctc ctt cag gct aac aga gac cct gat gct gga att gat gaa

528

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu

165

170

175

gct caa gtt gaa caa gat gct cag gct tta ttt cag gct gga gaa ctt

576

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu

180

185

190

aaa tgg ggg aca gat gaa gaa aag ttt atc acc atc ttt gga aca cga

624

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg

195

200

205

agt gtg tct cat ttg aga aag gtg ttt gac aag tac atg act ata tca

672

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser

210

215

220

gga ttt caa att gag gaa acc att gac cgc gag act tct ggc aat tta

720

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu

225

230

235

240

gag caa cta ctc ctt gct gtt gtg aaa tct att cga agt ata cct gcc

768

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala

245

250

255

tac ctt gca gag acc ctc tat tat gct atg aag gga gct ggg aca gat

816

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp

260

265

270

gat cat acc ctc atc aga gtc atg gtt tcc agg agt gag att gat ctg

864

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu

275

280

285

ttt aac atc agg aag gag ttt agg aag aat ttt gcc acc tct ctt tat

912

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr

290

295

300

tcc atg att aag gga gat aca tct ggg gac tat aag aaa gct ctt ctg

960

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu

305

310

315

320

ctg ctc tcc gga gaa gat gac

981

Leu Leu Ser Gly Glu Asp Asp

325

&lt;210&gt; 6

&lt;211&gt; 327

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 6

Met	Ala	Cys	Gly	Cys	Gly	His	Met	Ala	Gln	Val	Leu	Arg	Gly	Thr	Val
1				5					10					15	

Thr	Asp	Phe	Pro	Gly	Phe	Asp	Glu	Arg	Ala	Asp	Ala	Glu	Thr	Leu	Arg
			20					25					30		

Lys	Ala	Met	Lys	Gly	Leu	Gly	Thr	Asp	Glu	Glu	Ser	Ile	Leu	Thr	Leu
		35					40					45			

Leu	Thr	Ser	Arg	Ser	Asn	Ala	Gln	Arg	Gln	Glu	Ile	Ser	Ala	Ala	Phe
	50					55					60				

Lys Thr Leu Phe Gly Arg Asp Leu Leu Asp Asp Leu Lys Ser Glu Leu  
 65 70 75 80

Thr Gly Lys Phe Glu Lys Leu Ile Val Ala Leu Met Lys Pro Ser Arg  
 85 90 95

Leu Tyr Asp Ala Tyr Glu Leu Lys His Ala Leu Lys Gly Ala Gly Thr  
 100 105 110

Asn Glu Lys Val Leu Thr Glu Ile Ile Ala Ser Arg Thr Pro Glu Glu  
 115 120 125

Leu Arg Ala Ile Lys Gln Val Tyr Glu Glu Glu Tyr Gly Ser Ser Leu  
 130 135 140

Glu Asp Asp Val Val Gly Asp Thr Ser Gly Tyr Tyr Gln Arg Met Leu  
 145 150 155 160

Val Val Leu Leu Gln Ala Asn Arg Asp Pro Asp Ala Gly Ile Asp Glu  
 165 170 175

Ala Gln Val Glu Gln Asp Ala Gln Ala Leu Phe Gln Ala Gly Glu Leu  
 180 185 190

Lys Trp Gly Thr Asp Glu Glu Lys Phe Ile Thr Ile Phe Gly Thr Arg  
 195 200 205

Ser Val Ser His Leu Arg Lys Val Phe Asp Lys Tyr Met Thr Ile Ser  
 210 215 220

Gly Phe Gln Ile Glu Glu Thr Ile Asp Arg Glu Thr Ser Gly Asn Leu  
 225 230 235 240

Glu Gln Leu Leu Leu Ala Val Val Lys Ser Ile Arg Ser Ile Pro Ala  
 245 250 255

Tyr Leu Ala Glu Thr Leu Tyr Tyr Ala Met Lys Gly Ala Gly Thr Asp  
 260 265 270

Asp His Thr Leu Ile Arg Val Met Val Ser Arg Ser Glu Ile Asp Leu  
275 280 285

Phe Asn Ile Arg Lys Glu Phe Arg Lys Asn Phe Ala Thr Ser Leu Tyr  
290 295 300

Ser Met Ile Lys Gly Asp Thr Ser Gly Asp Tyr Lys Lys Ala Leu Leu  
305 310 315 320

Leu Leu Ser Gly Glu Asp Asp  
325

<210> 7  
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<212> DNA  
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<400> 7  
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21

<210> 8  
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<400> 8  
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21

<210> 9  
<211> 21  
<212> DNA  
<213> Homo sapiens

<400> 9  
tatggcaggt ggctgtggcc a  
21

<210> 10  
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<212> DNA

<213> Homo sapiens

<400> 10

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21

<210> 11

<211> 21

<212> DNA

<213> Homo sapiens

<400> 11

tatggcatgt ggctgcggtc a

21

<210> 12

<211> 21

<212> DNA

<213> Homo sapiens

<400> 12

tatgaccgca gccacatgcc a

21